

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently amended) A method for the expression of a nucleic acid sequence of interest in plant seeds, comprising: (a) preparing a chimeric nucleic acid construct comprising in the 5' to 3' direction of transcription as operably linked components: (1) a seed-specific promoter obtained from flax; and (2) said nucleic acid sequence of interest wherein said nucleic acid of interest is non-native to said seed-specific promoter; (b) introducing said chimeric nucleic acid construct into a plant cell; and (c) growing said plant cell into a mature plant capable of setting seed, wherein said nucleic acid sequence of interest is expressed in the seed under the control of said seed-specific promoter, and wherein said seed-specific promoter comprises a-an RY repeat and an ABRE promoter element ~~selected from the group of promoter elements consisting of RY repeat, ABRE, EBOX, and SEF3.~~

2. (Currently amended) ~~A-~~The method according to claim 1, wherein said plant seed is selected from the group of plants consisting of soybean (*Glycine max*), rapeseed (*Brassica napus*, *Brassica campestris*), sunflower (*Helianthus annuus*), cotton (*Gossypium hirsutum*), corn (*Zea mays*), tobacco (*Nicotiana tabacum*), alfalfa (*Medicago sativa*), wheat (*Triticum sp.*), barley (*Hordeum vulgare*), oats (*Avena sativa* L.), sorghum (*Sorghum bicolor*), *Arabidopsis thaliana*, potato (*Solanum sp.*), oil palm (*Eleais guineensis*), groundnut (*Arachis hypogaea*), Brazil nut (*Bertholletia excelsa*) coconut (*Cocus nucifera*), castor (*Ricinus communis*), coriander (*Coriandrum sativum*), squash (*Cucurbita maxima*), jojoba (*Simmondsia chinensis*) and rice (*Oryza sativa*).

3. (Currently amended) ~~A-~~The method according to claim 1, wherein said plant seed is flax/linseed (*Linum usitatissimum*).

4. (Currently amended) ~~A-The~~ method according to claim 1, wherein said plant seed is safflower (*Carthamus tinctorius*).

5-6. (Canceled).

7. (Currently amended) ~~A-The~~ method according to claim ~~6-1~~, wherein said RY repeat and ABRE promoter elements are separated from each other by less than 100 nucleotides and more than 20 nucleotides.

8. (Currently amended) ~~A-The~~ method according to claim ~~6-1~~, wherein said RY repeat and ABRE promoter elements are separated from each other by less than 50 nucleotides and more than 20 nucleotides.

9. (Currently amended) ~~A-The~~ method according to claim ~~6-1~~, wherein said RY repeat and ABRE promoter elements are separated from each other by less than 35 nucleotides and more than 20 nucleotides.

10. (Currently amended) ~~A-The~~ method according to claim ~~6-1~~, wherein said seed specific promoter obtained from flax additionally comprises an ~~E-Box~~ EBOX promoter element.

11. (Currently amended) ~~A-The~~ method according to claim 10, wherein said EBOX promoter element is between 250 to 150 nucleotides from the "ATG" start codon.

12. (Currently amended) ~~A-The~~ method according to claim 10, wherein said EBOX promoter element is between 200 to 175 nucleotides from the "ATG" start codon.

13. (Currently amended) ~~A-The~~ method according to claim 10, wherein said EBOX promoter element is between 195 to 185 nucleotides from the "ATG" start codon.

14. (Currently amended) ~~A-The~~ method according to claim ~~6-1~~, wherein said seed-

specific promoter obtained from flax additionally comprises an SEF3 promoter element.

15. (Currently amended) ~~A~~The method according to claim 14, wherein said SEF3 promoter element is, between 200 to 50 nucleotides from the "ATG" start codon.

16. (Currently amended) ~~A~~The method according to claim 14, wherein said SEF3 promoter element is between 175 to 100 nucleotides from the "ATG" start codon.

17. (Currently amended) ~~A~~The method according to claim 14, wherein said SEF3 promoter element is between 160 to 145 nucleotides from the "ATG" start codon.

18. (Currently amended) The method according to claim 1, wherein said flax seed-specific promoter comprises: (a) a nucleic acid sequence as shown in FIG. 1 (SEQ.ID.NO.:1) from nucleotides 1 to 2023, FIG. 2 (SEQ.ID.NO.:4) from nucleotides 1 to 1852, FIG. 3 (SEQ.ID.NO.:6) from nucleotides 1 to 417, or FIG. 4 (SEQ.ID.NO.:8) from nucleotides 1 to 2035, wherein T can also be U; (b) a nucleic acid sequence that is complementary to a nucleic acid sequence of (a); ~~(c) a nucleic acid sequence that has substantial sequence homology to a nucleic acid sequence of (a) or (b); (d) a nucleic acid sequence that is an analog of a nucleic acid sequence of (a), (b) or (c); or (e)~~ (c) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a), ~~(b), (c) or (d)~~ under stringent hybridization conditions which comprise hybridization at 5 x sodium chloride/sodium citrate (SSC) x Denhardt's solution/1.0% SDS at Tm -5°C, followed by a wash of 0.2 x SSC/0.1% SDS at 60°C.

19. (Currently amended) ~~Transgenic~~A transgenic plant capable of setting seed prepared by a method, comprising: (a) preparing a chimeric nucleic acid construct comprising in the 5' to 3' direction of transcription as operably linked components: (1) a seed-specific promoter obtained from flax; and (2) a nucleic ~~add~~acid sequence of interest wherein said nucleic acid of interest is non-native to said seed-specific promoter; (b) introducing said chimeric nucleic acid construct into a plant cell; and (c) growing said plant cell into a mature plant capable of

setting seed, wherein said nucleic acid sequence of interest is expressed in the seed under the control of said seed-specific promoter, and wherein said seed-specific promoter comprises a an RY repeat and an ABRE promoter element ~~selected from the group of promoter elements consisting of RY repeat, ABRE, EBOX, and SEF3.~~

20. (Currently amended) A-~~The~~ The transgenic plant according to claim 19, wherein said plant is selected from the group of plants consisting of soybean (*Glycine max*), rapeseed (*Brassica napus*, *Brassica campestris*), sunflower (*Helianthus annuus*), cotton (*Gossypium hirsutum*), corn (*Zea mays*), tobacco (*Nicotiana tabacum*), alfalfa (*Medicago sativa*), wheat (*Triticum sp.*), barley (*Hordeum vulgare*), oats (*Avena sativa* L.), sorghum (*Sorghum bicolor*), *Arabidopsis thaliana*, potato (*Solanum sp.*), oil palm (*Eleais guineensis*), groundnut (*Arachis hypogaea*), Brazil nut (*Bertholletia excelsa*) coconut (*Cocos nucifera*), castor (*Ricinus communis*), coriander (*Coriandrum sativum*), squash (*Cucurbita maxima*), jojoba (*Simmondsia chinensis*) and rice (*Oryza sativa*).

21. (Currently amended) A-~~The~~ The transgenic plant according to claim 19, wherein said plant is flax/linseed (*Linum usitatissimum*).

22. (Currently amended) A-~~The~~ The transgenic plant according to claim 19, wherein said plant is safflower (*Carthamus tinctorius*).

23-24. (Canceled).

25. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 19, wherein said RY repeat and ABRE promoter elements are separated from each other by less than 100 nucleotides and more than 20 nucleotides.

26. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 25, wherein said RY repeat and ABRE promoter elements are separated from each other by less than 50 nucleotides and more than 20 nucleotides.

27. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 25, wherein said RY repeat and ABRE promoter elements are separated from each other by less than 35 nucleotides and more than 20 nucleotides.
28. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 25, wherein said seed specific promoter obtained from flax additionally comprises an ~~E-Box~~ EBOX promoter element.
29. (Currently amended) ~~Transgenic~~ The transgenic plant to claim 28, wherein said EBOX promoter element is between 250 to 150 nucleotides from the "ATG" start codon.
30. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 28, wherein said EBOX promoter element is between 200 to 175 nucleotides from the "ATG" start codon.
31. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 28, wherein said EBOX promoter element is between 195 to 185 nucleotides from the "ATG" start codon.
32. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 25, wherein said seed-specific promoter obtained from flax additionally comprises an SEF3 promoter element.
33. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 32, wherein said SEF3 promoter element is between 200 to 50 nucleotides from the "ATG" start codon.
34. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 32, wherein said SEF3 promoter element is between 175 to 100 nucleotides from the "ATG" start codon.
35. (Currently amended) ~~Transgenic~~ The transgenic plant according to claim 32, wherein said SEF3 promoter element is between 160 to 145 nucleotides from the "ATG" start codon.

36-66. (Canceled).

67. (Currently amended) A plant prepared according to the method of claim ~~63~~1.

68. (Currently amended) A plant cell comprising ~~the a~~ chimeric nucleic acid sequence ~~according to claim 50~~ comprising (a) a first nucleic acid sequence comprising a seed-specific promoter obtained from flax which comprises a nucleic acid sequence comprising an RY repeat and an ABRE promoter element; and (b) a second nucleic acid sequence non-native to said flax seed-specific promoter.

69. (Currently amended) ~~A plant~~ Plant seed comprising ~~the a~~ chimeric nucleic acid sequence ~~according to claim 50~~ comprising (a) a first nucleic acid sequence comprising a seed-specific promoter obtained from flax which comprises a nucleic acid sequence comprising an RY repeat and an ABRE promoter element; and (b) a second nucleic acid sequence non-native to said flax seed-specific promoter.

70. (Currently amended) ~~Plant~~ A plant seed obtained from a plant prepared according to the method of claim ~~63~~1.

71. (Canceled).

72. (New) The transgenic plant according to claim 19, wherein said flax seed-specific promoter comprises: (a) a nucleic acid sequence as shown in FIG. 1 (SEQ.ID.NO.:1) from nucleotides 1 to 2023, FIG. 2 (SEQ.ID.NO.:4) from nucleotides 1 to 1852, FIG. 3 (SEQ.ID.NO.:6) from nucleotides 1 to 417, or FIG. 4 (SEQ.ID.NO.:8) from nucleotides 1 to 2035, wherein T can also be U; or (b) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a) under stringent hybridization conditions which comprise hybridization at 5 x sodium chloride/sodium citrate (SSC) x Denhardt's solution/1.0% SDS at T_m -5°C, followed by a wash of 0.2 x SSC/0.1% SDS at 60°C.

73. (New) The plant cell according to claim 68, wherein said flax seed-specific promoter comprises: (a) a nucleic acid sequence as shown in FIG. 1 (SEQ.ID.NO.:1) from nucleotides 1 to 2023, FIG. 2 (SEQ.ID.NO.:4) from nucleotides 1 to 1852, FIG. 3 (SEQ.ID.NO.:6) from nucleotides 1 to 417, or FIG. 4 (SEQ.ID.NO.:8) from nucleotides 1 to 2035, wherein T can also be U; or (b) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a) under stringent hybridization conditions which comprise hybridization at 5 x sodium chloride/sodium citrate (SSC) x Denhardt's solution/1.0% SDS at $T_m - 5^{\circ}\text{C}$, followed by a wash of 0.2 x SSC/0.1% SDS at 60°C .

74. (New) The plant cell according to claim 69, wherein said flax seed-specific promoter comprises: (a) a nucleic acid sequence as shown in FIG. 1 (SEQ.ID.NO.:1) from nucleotides 1 to 2023, FIG. 2 (SEQ.ID.NO.:4) from nucleotides 1 to 1852, FIG. 3 (SEQ.ID.NO.:6) from nucleotides 1 to 417, or FIG. 4 (SEQ.ID.NO.:8) from nucleotides 1 to 2035, wherein T can also be U; or (b) a nucleic acid sequence that hybridizes to a nucleic acid sequence of (a) under stringent hybridization conditions which comprise hybridization at 5 x sodium chloride/sodium citrate (SSC) x Denhardt's solution/1.0% SDS at $T_m - 5^{\circ}\text{C}$, followed by a wash of 0.2 x SSC/0.1% SDS at 60°C .